

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 5, 2006, 18:11:35 ; Search time 200 Seconds
(without alignments)
857.281 Million cell updates/sec

Title: US-10-092-934-10
Perfect score: 2034
Sequence: 1 MEFSLLLPRLECNGAISAHR.....FIRGGVSPYLSGWSQTPDLR 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2034	100.0	375	3	AAB01399	Aab01399 Neuron-as
2	2034	100.0	375	5	ABB81538	Abb81538 Neural th
3	2034	100.0	375	5	AAE29142	Aae29142 AD7c-NTP
4	2034	100.0	375	6	ABR63268	Abr63268 AD7c-NTP
5	2034	100.0	375	6	ADA84017	Ada84017 Human POM
6	2034	100.0	375	6	ABU03024	Abu03024 Human neu
7	2034	100.0	375	6	ABB99774	Abb99774 Amino aci
8	2034	100.0	375	6	ABJ19445	Abj19445 AD7C-neur
9	2034	100.0	375	7	ADB37642	Adb37642 Human neu
10	2034	100.0	375	8	ADR14409	Adr14409 Human NF-
11	2034	100.0	375	9	AEA30020	Aea30020 Human neu
12	1415.5	69.6	397	2	AAR95913	Aar95913 Neural th
13	928	45.6	381	4	AAU30235	Aau30235 Novel hum
14	927.5	45.6	382	4	AAU32610	Aau32610 Novel hum
15	927.5	45.6	382	4	AAU31818	Aau31818 Novel hum
16	927.5	45.6	382	4	AAU32707	Aau32707 Novel hum

17	849	41.7	324	4	AAU29573	Aau29573	Novel	hum
18	849	41.7	324	4	AAU29579	Aau29579	Novel	hum
19	822.5	40.4	411	4	ABG08428	Abg08428	Novel	hum
20	739	36.3	317	4	AAU33200	Aau33200	Novel	hum
21	735	36.1	290	4	ABG21913	Abg21913	Novel	hum
22	734.5	36.1	361	5	ABG68738	Abg68738	Human	pro
23	729	35.8	449	5	ABJ01057	Abj01057	Ovary	cel
24	701.5	34.5	332	5	ADK34410	Adk34410	Novel	hum
25	609	29.9	257	4	AAO10294	Aao10294	Human	pol
26	590	29.0	276	4	ABG07919	Abg07919	Novel	hum
27	575	28.3	302	5	ADK36936	Adk36936	Novel	hum
28	574	28.2	185	4	AAO06014	Aao06014	Human	pol
29	569	28.0	241	4	ABB11464	Abb11464	Human	neu
30	567.5	27.9	196	7	ADE09985	Ade09985	Novel	pro
31	563	27.7	202	4	AAU30686	Aau30686	Novel	hum
32	561	27.6	250	4	AAU31823	Aau31823	Novel	hum
33	561	27.6	250	7	ADE09441	Ade09441	Novel	pro
34	560	27.5	296	4	AAU33304	Aau33304	Novel	hum
35	554.5	27.3	232	5	ADK36978	Adk36978	Novel	hum
36	553	27.2	175	4	AAU31782	Aau31782	Novel	hum
37	550.5	27.1	215	4	AAU31513	Aau31513	Novel	hum
38	546	26.8	215	4	ABG07921	Abg07921	Novel	hum
39	543.5	26.7	216	4	AAU32615	Aau32615	Novel	hum
40	524	25.8	304	4	AAU30391	Aau30391	Novel	hum
41	522.5	25.7	175	4	AAU31857	Aau31857	Novel	hum
42	521.5	25.6	418	4	AAU31980	Aau31980	Novel	hum
43	520	25.6	396	4	AAU30455	Aau30455	Novel	hum
44	517	25.4	213	4	AAM25396	Aam25396	Human	pro
45	504.5	24.8	196	4	AAU31786	Aau31786	Novel	hum

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OM protein - protein search, using sw model

Run on: June 5, 2006, 18:29:46 ; Search time 50 Seconds
(without alignments)
656.480 Million cell updates/sec

Title: US-10-092-934-10
Perfect score: 2034
Sequence: 1 MEFSLLLPRLECNGAISAHR.....FIRGGVSPYLSGWSQTPDLR 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2034	100.0	375	1	US-08-454-557C-121	Sequence 121, App
2	2034	100.0	375	1	US-08-340-426D-121	Sequence 121, App
3	2034	100.0	375	1	US-08-450-673C-121	Sequence 121, App
4	2034	100.0	375	2	US-09-872-968-2	Sequence 2, Appli
5	2034	100.0	375	2	US-10-153-334-1	Sequence 1, Appli
6	1415.5	69.6	397	5	PCT-US95-17111A-121	Sequence 121, App
7	377.5	18.6	158	2	US-10-104-047-3047	Sequence 3047, Ap
8	324	15.9	189	2	US-10-104-047-3196	Sequence 3196, Ap
9	310	15.2	101	2	US-10-094-749-2181	Sequence 2181, Ap
10	307	15.1	114	2	US-10-104-047-2423	Sequence 2423, Ap
11	301	14.8	156	2	US-10-104-047-2334	Sequence 2334, Ap
12	299.5	14.7	176	2	US-10-094-749-2950	Sequence 2950, Ap
13	283.5	13.9	110	2	US-10-104-047-3422	Sequence 3422, Ap
14	283	13.9	123	2	US-10-104-047-2112	Sequence 2112, Ap
15	280	13.8	152	2	US-10-104-047-2372	Sequence 2372, Ap
16	267.5	13.2	96	2	US-09-513-999C-6065	Sequence 6065, Ap
17	262	12.9	46	2	US-10-153-334-48	Sequence 48, Appl
18	261.5	12.9	128	2	US-10-104-047-2789	Sequence 2789, Ap
19	259.5	12.8	144	2	US-09-513-999C-6953	Sequence 6953, Ap

20	258	12.7	129	2	US-10-104-047-2565	Sequence 2565, Ap
21	256	12.6	108	2	US-09-513-999C-7878	Sequence 7878, Ap
22	254.5	12.5	239	2	US-09-800-729-193	Sequence 193, App
23	254.5	12.5	310	2	US-09-800-729-190	Sequence 190, App
24	253	12.4	118	2	US-09-663-600A-114	Sequence 114, App
25	252.5	12.4	110	2	US-10-104-047-2974	Sequence 2974, Ap
26	251.5	12.4	113	2	US-10-094-749-2649	Sequence 2649, Ap
27	251	12.3	776	2	US-10-020-079-24	Sequence 24, Appl
28	251	12.3	776	2	US-10-413-437-24	Sequence 24, Appl
29	251	12.3	789	2	US-10-020-079-22	Sequence 22, Appl
30	251	12.3	789	2	US-10-413-437-22	Sequence 22, Appl
31	251	12.3	863	2	US-10-020-079-32	Sequence 32, Appl
32	251	12.3	863	2	US-10-413-437-32	Sequence 32, Appl
33	251	12.3	876	2	US-10-020-079-30	Sequence 30, Appl
34	251	12.3	876	2	US-10-413-437-30	Sequence 30, Appl
35	251	12.3	889	2	US-10-020-079-20	Sequence 20, Appl
36	251	12.3	889	2	US-10-413-437-20	Sequence 20, Appl
37	251	12.3	895	2	US-10-020-079-18	Sequence 18, Appl
38	251	12.3	895	2	US-10-413-437-18	Sequence 18, Appl
39	251	12.3	976	2	US-10-020-079-28	Sequence 28, Appl
40	251	12.3	976	2	US-10-413-437-28	Sequence 28, Appl
41	251	12.3	982	2	US-10-020-079-26	Sequence 26, Appl
42	251	12.3	982	2	US-10-413-437-26	Sequence 26, Appl
43	250	12.3	97	2	US-09-513-999C-4770	Sequence 4770, Ap
44	250	12.3	100	2	US-10-094-749-3044	Sequence 3044, Ap
45	250	12.3	132	2	US-09-636-215-573	Sequence 573, App

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OM protein - protein search, using sw model

Run on: June 5, 2006, 18:41:47 ; Search time 185 Seconds
(without alignments)
938.949 Million cell updates/sec

Title: US-10-092-934-10
Perfect score: 2034
Sequence: 1 MEFSLLLPRLECNGAISAHR.....FIRGGVSPYLSGWSQTPDLR 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2034	100.0	375	3	US-09-964-666-2	Sequence 2, Appli
2	2034	100.0	375	3	US-09-964-412-2	Sequence 2, Appli
3	2034	100.0	375	3	US-09-964-667-2	Sequence 2, Appli
4	2034	100.0	375	3	US-09-872-968-2	Sequence 2, Appli
5	2034	100.0	375	3	US-09-964-678A-2	Sequence 2, Appli
6	2034	100.0	375	4	US-10-146-130-2	Sequence 2, Appli
7	2034	100.0	375	4	US-10-092-934-10	Sequence 10, Appl
8	2034	100.0	375	4	US-10-153-334-1	Sequence 1, Appli
9	2034	100.0	375	4	US-10-198-069-1	Sequence 1, Appli
10	2034	100.0	375	4	US-10-157-031-299	Sequence 299, App
11	2034	100.0	375	4	US-10-198-070-1	Sequence 1, Appli
12	2034	100.0	375	4	US-10-755-889-410	Sequence 410, App
13	2034	100.0	375	5	US-10-910-173-2	Sequence 2, Appli
14	822.5	40.4	411	5	US-10-450-763-38787	Sequence 38787, A
15	735	36.1	290	5	US-10-450-763-52272	Sequence 52272, A
16	734.5	36.1	361	3	US-09-995-494-107	Sequence 107, App
17	729	35.8	449	4	US-10-007-280A-140	Sequence 140, App
18	590	29.0	276	5	US-10-450-763-38278	Sequence 38278, A
19	569	28.0	241	4	US-10-276-774-1834	Sequence 1834, Ap
20	546	26.8	215	5	US-10-450-763-38280	Sequence 38280, A

21	517	25.4	213	4	US-10-296-115-911	Sequence 911, App
22	471	23.2	286	4	US-10-291-172-654	Sequence 654, App
23	471	23.2	286	4	US-10-221-278-654	Sequence 654, App
24	464	22.8	154	5	US-10-450-763-38784	Sequence 38784, A
25	457.5	22.5	264	5	US-10-450-763-52437	Sequence 52437, A
26	428.5	21.1	183	3	US-09-989-920-245	Sequence 245, App
27	427	21.0	146	5	US-10-450-763-38554	Sequence 38554, A
28	407	20.0	361	4	US-10-276-774-1862	Sequence 1862, Ap
29	382.5	18.8	341	5	US-10-220-335-586	Sequence 586, App
30	382.5	18.8	673	4	US-10-157-031-291	Sequence 291, App
31	377.5	18.6	158	4	US-10-104-047-3047	Sequence 3047, Ap
32	377.5	18.6	158	6	US-11-072-512-3047	Sequence 3047, Ap
33	365.5	18.0	126	5	US-10-450-763-38786	Sequence 38786, A
34	356.5	17.5	603	4	US-10-408-765A-140	Sequence 140, App
35	353.5	17.4	217	4	US-10-017-161-1956	Sequence 1956, Ap
36	353.5	17.4	217	4	US-10-292-798-1604	Sequence 1604, Ap
37	349	17.2	157	4	US-10-108-260A-4272	Sequence 4272, Ap
38	336	16.5	148	4	US-10-276-774-1784	Sequence 1784, Ap
39	332	16.3	108	4	US-10-078-090-143	Sequence 143, App
40	328.5	16.2	252	5	US-10-450-763-33745	Sequence 33745, A
41	324	15.9	189	4	US-10-104-047-3196	Sequence 3196, Ap
42	324	15.9	189	6	US-11-072-512-3196	Sequence 3196, Ap
43	317	15.6	122	5	US-10-450-763-38275	Sequence 38275, A
44	316	15.5	152	4	US-10-198-070-112	Sequence 112, App
45	311	15.3	74	4	US-10-276-774-1929	Sequence 1929, Ap

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OM protein - protein search, using sw model

Run on: June 5, 2006, 18:42:11 ; Search time 16 Seconds
(without alignments)
271.058 Million cell updates/sec

Title: US-10-092-934-10
Perfect score: 2034
Sequence: 1 MEFSLLLPRLECNGAISAHR.....FIRGGVSPYLSGWSQTPDLR 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	349	17.2	157	7	US-11-293-697-4272	Sequence 4272, Ap
2	303	14.9	203	7	US-11-293-697-2748	Sequence 2748, Ap
3	290.5	14.3	127	7	US-11-293-697-2558	Sequence 2558, Ap
4	287	14.1	180	7	US-11-293-697-4793	Sequence 4793, Ap
5	274	13.5	125	7	US-11-293-697-4066	Sequence 4066, Ap
6	262.5	12.9	100	7	US-11-293-697-3143	Sequence 3143, Ap
7	262.5	12.9	179	7	US-11-293-697-4646	Sequence 4646, Ap
8	261	12.8	140	7	US-11-293-697-2547	Sequence 2547, Ap
9	260.5	12.8	273	7	US-11-293-697-2884	Sequence 2884, Ap
10	258.5	12.7	140	7	US-11-293-697-4151	Sequence 4151, Ap
11	257	12.6	134	7	US-11-293-697-4651	Sequence 4651, Ap
12	256	12.6	138	7	US-11-293-697-4194	Sequence 4194, Ap
13	252.5	12.4	108	7	US-11-293-697-4789	Sequence 4789, Ap
14	249	12.2	116	7	US-11-293-697-2525	Sequence 2525, Ap
15	248	12.2	440	6	US-10-196-749-386	Sequence 386, App
16	248	12.2	440	7	US-11-101-316-134	Sequence 134, App
17	247.5	12.2	630	7	US-11-293-697-4498	Sequence 4498, Ap
18	242.5	11.9	204	7	US-11-293-697-3687	Sequence 3687, Ap

19	240	11.8	216	7	US-11-293-697-4836	Sequence 4836, Ap
20	239	11.8	105	7	US-11-293-697-3988	Sequence 3988, Ap
21	233.5	11.5	129	7	US-11-293-697-2565	Sequence 2565, Ap
22	230.5	11.3	108	7	US-11-293-697-3308	Sequence 3308, Ap
23	229.5	11.3	118	7	US-11-293-697-4243	Sequence 4243, Ap
24	222	10.9	114	7	US-11-293-697-3855	Sequence 3855, Ap
25	221	10.9	128	7	US-11-293-697-4222	Sequence 4222, Ap
26	221	10.9	136	7	US-11-293-697-2898	Sequence 2898, Ap
27	220.5	10.8	111	7	US-11-293-697-2465	Sequence 2465, Ap
28	219	10.8	166	7	US-11-293-697-2532	Sequence 2532, Ap
29	219	10.8	228	7	US-11-293-697-2562	Sequence 2562, Ap
30	217	10.7	104	7	US-11-293-697-2906	Sequence 2906, Ap
31	216	10.6	109	7	US-11-293-697-4725	Sequence 4725, Ap
32	215.5	10.6	101	7	US-11-293-697-4884	Sequence 4884, Ap
33	215.5	10.6	129	7	US-11-293-697-4783	Sequence 4783, Ap
34	209	10.3	108	7	US-11-293-697-4235	Sequence 4235, Ap
35	207	10.2	117	7	US-11-293-697-2879	Sequence 2879, Ap
36	206.5	10.2	101	7	US-11-293-697-2539	Sequence 2539, Ap
37	205.5	10.1	101	7	US-11-293-697-2559	Sequence 2559, Ap
38	201.5	9.9	115	7	US-11-293-697-3605	Sequence 3605, Ap
39	199	9.8	120	7	US-11-293-697-4121	Sequence 4121, Ap
40	198.5	9.8	127	7	US-11-293-697-4007	Sequence 4007, Ap
41	197.5	9.7	113	7	US-11-293-697-3204	Sequence 3204, Ap
42	197	9.7	138	7	US-11-293-697-3556	Sequence 3556, Ap
43	195.5	9.6	106	7	US-11-293-697-4581	Sequence 4581, Ap
44	193	9.5	105	7	US-11-293-697-4709	Sequence 4709, Ap
45	190.5	9.4	100	7	US-11-293-697-3335	Sequence 3335, Ap

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OM protein - protein search, using sw model

Run on: June 5, 2006, 18:24:45 ; Search time 40 Seconds
(without alignments)
902.032 Million cell updates/sec

Title: US-10-092-934-10
Perfect score: 2034
Sequence: 1 MEFSLLLPRLECNGAISAHR.....FIRGGVSPYLSGWSQTPDLR 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	382.5	18.8	673	4	F40201	artifact-warning s
2	315.5	15.5	613	4	C40201	artifact-warning s
3	315.5	15.5	627	4	A40201	artifact-warning s
4	291.5	14.3	597	4	E40201	artifact-warning s
5	197.5	9.7	579	4	D40201	artifact-warning s
6	175	8.6	499	2	S65657	alpha-1C-adrenergi
7	167	8.2	46	2	I54375	gene NF2 protein -
8	161	7.9	841	1	I78885	serine/threonine-s
9	157	7.7	39	2	I54374	gene NF2 protein -
10	151.5	7.4	301	4	B40201	artifact-warning s
11	139.5	6.9	100	2	A46010	X-linked retinopat
12	137.5	6.8	79	2	A56194	thromboxane A-2 re
13	137.5	6.8	407	2	T02670	probable thromboxa
14	128	6.3	53	2	A42442	integrin beta-1 ch
15	112	5.5	440	2	A26359	decay-accelerating
16	106.5	5.2	1125	2	T19193	hypothetical prote
17	105	5.2	522	2	T08711	gamma-adaptin homo
18	102.5	5.0	331	2	S59501	interferon recepto
19	99.5	4.9	331	2	A54295	interferon alpha/b
20	96.5	4.7	1643	1	RRWGNV	genome polyprotein
21	96	4.7	458	2	E82175	conserved hypothet
22	92	4.5	964	2	T15342	hypothetical prote

23	91.5	4.5	542	2	S39608	transcription fact
24	91.5	4.5	631	1	A36749	transcription fact
25	91.5	4.5	1776	1	RRWPYM	genome polyprotein
26	90.5	4.4	282	1	SAVL64	middle surface ant
27	90.5	4.4	832	1	S20752	DNA-directed DNA p
28	90	4.4	431	1	SAVLC2	large surface anti
29	89	4.4	299	2	F84785	probable xylogluca
30	89	4.4	333	2	AI2131	hypothetical prote
31	89	4.4	1162	2	B97852	hypothetical prote
32	88	4.3	209	2	JC4244	heat-shock 27K pro
33	88	4.3	726	2	S18208	rabphilin-3A-inter
34	88	4.3	832	2	S71785	DNA-directed DNA p
35	87.5	4.3	494	2	S39607	transcription fact
36	87	4.3	226	1	JQ1574	major surface anti
37	87	4.3	226	2	JQ2101	surface antigen -
38	87	4.3	470	2	T05258	glycine hydroxymet
39	87	4.3	1153	2	A49676	nitric-oxide synth
40	86.5	4.3	360	2	T45956	hypothetical prote
41	86.5	4.3	1886	2	S04921	nuclear pore prote
42	86	4.2	262	2	AF2291	hypothetical prote
43	86	4.2	625	2	E96721	hypothetical prote
44	85.5	4.2	832	1	JDVLA1	DNA-directed DNA p
45	84.5	4.2	191	2	C72455	hypothetical prote

SCORE Search Results Details for Application 10092934
and Search Result us-10-092-934-10.rup.

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OM protein - protein search, using sw model

Run on: June 5, 2006, 18:21:40 ; Search time 297 Seconds
(without alignments)
1167.949 Million cell updates/sec

Title: US-10-092-934-10
Perfect score: 2034
Sequence: 1 MEFSLLLPRLECNGAISAHR.....FIRGGVSPYLSGWSQTPDLR 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2034	100.0	375	2	O60448_HUMAN	O60448 homo sapien
2	595	29.3	587	1	ALU2_HUMAN	P39189 homo sapien
3	568	27.9	587	1	ALU3_HUMAN	P39190 homo sapien
4	549.5	27.0	591	1	ALU8_HUMAN	P39195 homo sapien
5	498.5	24.5	591	1	ALU1_HUMAN	P39188 homo sapien
6	389	19.1	585	1	ALU5_HUMAN	P39192 homo sapien
7	377.5	18.6	158	2	Q8NAL9_HUMAN	Q8nal9 homo sapien
8	357.5	17.6	593	1	ALU6_HUMAN	P39193 homo sapien
9	356.5	17.5	603	1	ALU4_HUMAN	P39191 homo sapien
10	349	17.2	157	2	Q8N845_HUMAN	Q8n845 homo sapien
11	337.5	16.6	164	2	Q6ZTS0_HUMAN	Q6zts0 homo sapien

12	332	16.3	176	2	Q6ZR92_HUMAN	Q6zr92	homo sapien
13	331	16.3	170	2	Q6ZVI4_HUMAN	Q6zvi4	homo sapien
14	330.5	16.2	593	1	ALU7_HUMAN	P39194	homo sapien
15	325	16.0	143	2	Q6ZSJ7_HUMAN	Q6zsj7	homo sapien
16	320	15.7	195	2	Q6ZUW2_HUMAN	Q6zuw2	homo sapien
17	316	15.5	152	2	Q9NX85_HUMAN	Q9nx85	homo sapien
18	303.5	14.9	239	2	Q6ZWA9_HUMAN	Q6zwa9	homo sapien
19	303	14.9	124	2	Q6ZVF6_HUMAN	Q6zvf6	homo sapien
20	301	14.8	156	2	Q8N266_HUMAN	Q8n266	homo sapien
21	295	14.5	193	2	Q6ZVX8_HUMAN	Q6zvx8	homo sapien
22	294.5	14.5	148	2	Q6ZUC5_HUMAN	Q6zuc5	homo sapien
23	290	14.3	123	2	Q6ZV58_HUMAN	Q6zv58	homo sapien
24	287.5	14.1	166	2	Q6ZUC0_HUMAN	Q6zuc0	homo sapien
25	287	14.1	180	2	Q8N7M7_HUMAN	Q8n7m7	homo sapien
26	286.5	14.1	130	2	Q6ZSV2_HUMAN	Q6zsv2	homo sapien
27	286.5	14.1	131	2	Q6ZTD3_HUMAN	Q6ztd3	homo sapien
28	283	13.9	125	2	Q6ZTE1_HUMAN	Q6zte1	homo sapien
29	281.5	13.8	147	2	Q6ZUA2_HUMAN	Q6zua2	homo sapien
30	280	13.8	165	2	Q6ZTF6_HUMAN	Q6ztf6	homo sapien
31	279.5	13.7	132	2	Q6ZS28_HUMAN	Q6zs28	homo sapien
32	279	13.7	142	2	Q6ZWD5_HUMAN	Q6zwd5	homo sapien
33	277	13.6	145	2	Q4R5J6_MACFA	Q4r5j6	macaca fasc
34	276	13.6	129	2	Q6ZW43_HUMAN	Q6zw43	homo sapien
35	274	13.5	125	2	Q8N8C2_HUMAN	Q8n8c2	homo sapien
36	274	13.5	164	2	Q6ZUK0_HUMAN	Q6zuk0	homo sapien
37	273.5	13.4	118	2	Q9H387_HUMAN	Q9h387	homo sapien
38	272	13.4	140	2	Q6ZU13_HUMAN	Q6zul3	homo sapien
39	271	13.3	121	2	Q6ZQS8_HUMAN	Q6zqs8	homo sapien
40	269	13.2	137	2	Q6ZS97_HUMAN	Q6zs97	homo sapien
41	269	13.2	241	2	Q6ZTY3_HUMAN	Q6zty3	homo sapien
42	268.5	13.2	129	2	Q6ZUW8_HUMAN	Q6zuw8	homo sapien
43	268	13.2	260	2	Q6ZQR8_HUMAN	Q6zqr8	homo sapien
44	267.5	13.2	165	2	Q6ZS53_HUMAN	Q6zs53	homo sapien
45	267.5	13.2	165	2	Q6ZT71_HUMAN	Q6zt71	homo sapien

ALIGNMENTS

RESULT 1

O60448_HUMAN

ID O60448_HUMAN PRELIMINARY; PRT; 375 AA.

AC O60448;

DT 01-AUG-1998, integrated into UniProtKB/TrEMBL.

DT 01-AUG-1998, sequence version 1.

DT 07-FEB-2006, entry version 15.

DE Neuronal thread protein AD7c-NTP.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Neuronal;

RX MEDLINE=98064067; PubMed=9399956;

RA Monte S.M., Ghanbari K., Frey W.H., Beheshti I., Averbach P.,

RA Hauser S.L., Ghanbari H.A., Wands J.R.;

RT "Characterization of the AD7C-NTP cDNA expression in Alzheimer's disease and measurement of a 41-kD protein in cerebrospinal fluid.";

RL J. Clin. Invest. 100:3093-3104(1997).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Neuronal;

RA de la Monte S.M., Wands J.R.;